RAW SEQUENCE LISTING PATENT APPLICATION US/08/487,032

DATE: 02/23/96 TIME: 11:34:47

INPUT SET: S8924.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

	1	SEQUENCE LISTING
	2	(1) Ganamal Tufannakian
	3	(1) General Information:
	4 5 6	(i) APPLICANT: DOUGLAS SMITH
	7	(ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
	8	RELATING TO HELICOBACTER PYLORI FOR
	9	DIAGNOSTICS AND THERAPEUTICS
	10	DIAGNOSTICS AND THERAPEUTICS
>	11	(iii) NUMBER OF SEQUENCES: 880
	12	(III) NORDER OF DEGOENCES. GOV
	13	(iv) CORRESPONDENCE ADDRESS:
	14	(A) ADDRESSEE: LAHIVE & COCKFIELD
	15	(IV) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: LAHIVE & COCKFIELD (B) STREET: 60 State Street, Suite 510 (C) CITY: Boston
	16	(C) CITY: Boston
	17	(D) STATE: Massachusetts
	18	(E) COUNTRY: USA
	19	(F) ZIP: 02109-1875
	20	
	21	(V) COMPUTER READABLE FORM:
	22	(A) MEDIUM TYPE: Floppy disk
	23	(B) COMPUTER: IBM PC compatible
	24	(C) OPERATING SYSTEM: PC-DOS/MS-DOS
	25	(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
	26	
	27	(vi) CURRENT APPLICATION DATA:
	28	(A) APPLICATION NUMBER: US 08/487,032
	29	(B) FILING DATE: 07-JUNE-1995
	30	
	31	(viii) ATTORNEY/AGENT INFORMATION:
	32	(A) NAME: Mandragouras, Amy E.
	33	(B) REGISTRATION NUMBER: 36,207
	34	(C) REFERENCE/DOCKET NUMBER: GTN-001
	35	
	36	(ix) TELECOMMUNICATION INFORMATION:
	37	(A) TELEPHONE: (617)227-7400
	38	(B) TELEFAX: (617)227-5941
	39	

ERRORED SEQUENCES FOLLOW:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/487,032

DATE: 02/23/96 TIME: 11:34:52

			INPU1 SE1: 38924.raw
	5923	(2) INFORMATION FOR SEQ ID NO:149:	
	5924		
	5925	(i) SEQUENCE CHARACTERISTICS:	
	5926	(A) LENGTH: 1017 base pairs	
	5927	(B) TYPE: nucleic acid	
	5928 5929	<pre>(C) STRANDEDNESS: double (D) TOPOLOGY: circular</pre>	•
	5929	(D) TOPOLOGY: CIrcular	
	5931	(ii) MOLECULE TYPE: DNA (genomic)	
	5932	(11) Modecode 11ra. DAR (genomic)	
	5933	(iii) HYPOTHETICAL: NO	•
	5934		
	5935	(iv) ANTI-SENSE: NO	
	5936	, ,	o ' - act
	5937	(vi) ORIGINAL SOURCE:	() insert
	5938	(A) ORGANISM: Helicobacter pylori	T
	5939		SEG ID NO:149
	5940		
	5941		
->	5942	(xi) SEQUENCE DESCRIPTION: PHOSPHOMANNO	:UTASE:
	5943 5944	AMONTO COMOTO COMOTO CARA COMO COMO COMO COMO COMO COMO COMO COM	
	5944 5945	ATGATCACTG GCTCTCACAA CCCCAAAGAA TACAACGGCT	TTAAAATCAC GCTCAATCAA 60
	5945 5946	AACCCGTTTT ATGGCAAGGA CATTCAGGCT TTAAAAAACA	A COCOMMUNA A COCA A A COCA M
	5947	AACCCGITIT AIGGCAAGGA CAITCAGGCT TTAAAAAACA	A CGCTTTTAAA CGCAAAGCAT 120
	5948	GAAATAAAGC CCCTAAAAGA AACGCCAGAG AAAGTCAATG	CCCTAGAAGC GTATCATCGC 180
	5949	OMMINATO COCIMANON ANCOCCACAO AMOICANIC	CCCIAGRAGE GIAICAICGE 100
	5950	TATTTGATCA AGGATTTTAA GCATTTAAAA AATCTTAAAT	ACAAAATCGC CCTGGATTTT 240
	5951		
	5952	GGTAATGGCG TGGGGGCGTT AGGATTAGAG CCGATTTTAA	A AGGCTTTAAA CATTGATTTT 300
	5953		
	5954	AGCAGCCTTT ATAGCGATCC TGATGGGGAT TTTCCTAACC	C ACCACCCAGA CCCTAGCGAA 360
	5955		
	5956	GCGAAAAACT TAAAAGACTT AGAAAAACAC ATGCGAGAAA	A ACGCTATTTT AATAGGCTTT 420
	5957		
	5958 5959	GCTTTTGATG GCGATGCGGA TAGGATTGCG ATGCTAAGCT	CTCATCATAT CTATGCGGGC 480
	5960	GATGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC	1
	5961	GAIGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC	C AAGGCATCAC CCCTTTTGTG 540
	5962	ATCGGCGAAG TCAAATGCTC TCAAGTGATG TATAACGCAA	TCAATACTTT TGGTAAGACG 600
	5963	interesting tolking tolker tolker	TORRINGITI IGGIRRONCG UU
	5964	CTCATGTATA AAACCGGGCA TAGCAATTTA AAAATCAAGC	TCAAAGAAAC TAATGCGCAT 660
	5965		
	5966	TTTGCGGCTG AAATGAGCGG GCATATCTTT TTTAAAGAAC	GCTATTTTGG CTATGATGAC 720
	5967		
	5968	GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG	AACAAAGTCC AAGCGACTTG 780
	5969		
	5970	GAAAACACCA TTAAAAACCT CCCCTATTCC TACACCACGC	CTGAAGAAAA AATCGCCGTG 840
	5971		
	5972	AGCGAAGAAG AAAAATTTGA AATCATTCGC AACTTACAAG	S AAGCGCTTAA AAACCCGCCA 900
	5973	ACCOMMUNICA CONTRATA TOTAL TOT	
	5974	AGCCATTTCC CTACAATCAA AGAAATCATC AGCATTGATG	G GCGTGAGAGT GGTTTTTGAA 960
	5975		

RAW SEQUENCE LISTING PATENT APPLICATION US/08/487,032

DATE: 02/23/96 TIME: 11:34:56

	5976 5977 5978	CATGGCTTTG GGCTTATTCG CGCAAGCAAC ACCCACCCC TATTTAGTCA GCCGCTT 1017
	7253	(2) INFORMATION FOR SEQ ID NO:179: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 264 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: circular (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Helicobacter pylori (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179: GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA 60
	7254	(
	7255	(i) SEQUENCE CHARACTERISTICS:
>	7256	(A) LENGTH: 264 base pairs
	7257	(B) TYPE: nucleic acid
	7258	(C) STRANDEDNESS: double
	7259	(D) TOPOLOGY: circular
	7260	(it) NOT FOUR THE PARTY OF AN INC.
	7261	(ii) MOLECULE TYPE: DNA (genomic)
	7262 7263	(iii) Hypomummaaa ayo
	7263 7264	(iii) HYPOTHETICAL: NO
	7265	(iv) ANTI-SENSE: NO
	7266	(IV) ANTI-SENSE: NO
	7267	(vi) ORIGINAL SOURCE:
	7268	(A) ORGANISM: Helicobacter pylori
	7269	loo you
	7270	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:
	7271	
	7272	GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA 60
	7273	·
	7274	GGGGTGTTGT TAGCATGTTT TTATCTTTTA GACGCTTATT ATCTCATGCA AGAAAGGCTG 120
	7275	
	7276	TTTAGGGAGC AATACCAATG GCTAATAAAA AACCGACTTA AAACCGATGA AAGGCTGTTT 180
	7277	
	7278	GAAGTCTTCC CTATTCATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCGTTCGT 240
	7279	
	7280 7281	TTAGTCTTTT CCCCTATTGG GCGT . \$%(,, La j (Ia H A P T (D ! E S J AgI) b dvOL FH ig acid
	7281 7282	H A P T (D!E\$JAqI1 b dvQL_FHiq acid (C) STRANDEDNESS: double
>	7282	(D) TOPOLOGY: circular
	7284	(b) loronogi, ciiculai
	7285	(ii) MOLECULE TYPE: DNA (genomic)
	7286	(11) 11011101111111111111111111111111111
	7287	(iii) HYPOTHETICAL: NO
	7288	7
	7289	(iv) ANTI-SENSE: NO
	7290	V. V.
>	7291	(vi) O NâOTAAAGCGGTC 240
	7292	
	7293	TTTTTCACCC ACCATACTTT AAAGGCTTCG TTTGAGCCGA CTAACCACAT CAATTATAGA 300
	7294	
	7295	GGGCATGACT ATGTGTTGGA TAATGTGCAT TTCCACGCCC CTATGGAGTT TTTAATCAAT 360
	7296	
	7297	AATAAAACCA GGCCTTTGAG CGCGCATTTC GTGCATAAAG ACGCTAAAGG GCGTTTGTTG 420
	7298	CMCMM3.0003
	7299 7300	GTGTTAGCGA TTGGTTTTGA AGAAGGGAAA GAAAACCCCA ACCTTGATCC TATTTTAGAA 480
	7300	GGCATTCAAA AGAAACAAAA TCTTAAAGAG GTGGCTTTAG ACGCTTTCTT GCCTAAAAGC 540
	/301	GGCATTCAAA AGAAACAAAA TCTTAAAGAG GTGGCTTTAG ACGCTTTCTT GCCTAAAAAGC 540

RAW SEQUENCE LISTING PATENT APPLICATION US/08/487,032

DATE: 02/23/96 TIME: 11:35:00

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	7303	ATCAATTACT ACCATTTTAA CGGCTCTCTC ACCGCTCCTC CTTGCACAGA GGGGGTGGCA 6	00
	7304		
	7305	TGGTTTGTCA TAGAAGAACC TTTGGAAGTT TCTGCCAAAC AATTGGCTGA AATCAAAAAA 6	60
	7306		
	7307	CGCATGAAAA ATTCGCCCAA CCAACGCCCC GTCCAGCCTG ACTACAACAC CGTGATCATT 7	20
	7308		
	7309	AAAAGCTCGG CTGAGACCCG C 7	41
,	7310		
	7311		
>	7312	(2) INFORMATION FOR SEQ ID NO:131:	
/	7312	(2) INFORMATION FOR SEQ ID NO:131: JUmps 131	
	7313	(i) SEQUENCE CHARACTERISTICS:	
	7315	(A) LENGTH: 1266 base pairs	
	7316	(B) TYPE: nucleic acid	
	7317	(C) STRANDEDNESS: double	
	7318	(D) TOPOLOGY: circular	
	7319	(-,	
	7320	(ii) MOLECULE TYPE: DNA (genomic)	
	7321		
	7322	(iii) HYPOTHETICAL: NO	
	7323		
	7324	(iv) ANTI-SENSE: NO	
	7325	·	•
	7326	(vi) ORIGINAL SOURCE:	
	7327	(A) ORGANISM: Helicobacter pylori	
	7328		
	7329	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:	
	7330		
	7331	ATGAAAATTT CTTTATTGGG GCATGGAAAA ACCACTCTAG CCCTAGGGCG TTTTTTTAAA	60
	7332	11111G1M1 1MG11GMG11 1MMMMMMG1M G1M111MMGG GMGG1MMMMM M11GG1M1GG	00
	7333 7334	AAAAACCATA ATGAAGTCAA ATTTTTTGAT GATAAATTCC CTGCATTTTT TAAGGATAGC 1	20
	7334	GAGGGTTTTC TTTGCTACCC TAGTAAGGAT TTTAACCCTA ATGATTCCCA ACTAGAAATC 1	80
	7336	ondodilite illidelacce ladianddal lllanceela aldalleeca acladaale	00
	7337	GTCAGCCCTG GCATTAGTTT CACGCACCCT TTAGTCATGA AAGCCAAGCA TTTAATGAGC 2	40
	7338		••
	7339	GAATACGATT ATATTGATAG TTTGTTTGAT CATTCTTTCA CGCCTACGAT GATAAGTATT 3	00
	7340		
	7341	AGCGGCACTA ACGGGAAAAC CACCACGACC GAAATGCTCA CCACACTTTT AGAAGATTTT 3	60
	7342		
	7343	AAGGCTGTGA GTGGGGGGAA TATCGGCACG CCCTTGATTG AATTGTTTGA AAAACGATCG 4	20
	7344		
	7345	CCCTTGTGGG TGCTAGAAAC AAGCTCCTTT TCTTTGCATT ACACTAATAA GGCTTACCCT 4	80
	7346		
	7347	TTAATCTACT TGCTCATCAA TGTGGAAGCC GATCATTTGA CTTGGCATTG CAATTTTGAA 5	40
	7348		• •
	7349	AATTATTTGA ACGCTAAACT CAAGGTTTTA ACATTGATGC CTAAAACTTC GCTCGCTATC 6	00
	7350	CMCGCMMM11 11MMC111C1 101CCCM1MM CMCC111CM CCC11CCCC1 11111MAMM	. 0
	7351	CTCCCTTTAA AATTCAAAGA ACACCCTATT GTTCAAAACT CGCAAGCGCA AAAAATCTTT 6	60
	7352	######################################	20
	7353	TTTGACAAAA GCGAAGAGGT TTTAGAGTGT TTAAAAAATCC CTTCTAACGC CCTTTTTTTT 7	20

RAW SEQUENCE LISTING PATENT APPLICATION US/08/487,032

DATE: 02/23/96 TIME: 11:35:04

SEQ ID NO: 149:

7354			•		i	INPUT SET: S8924.rd	aw.
7355	AAGGGAGCGT	TTTTATTAGA	CGCGGCTTTA	GCCCTTTTAG	TTTATGAGCA	АТТТТАААА	780
7356 7357	ATAAAGAATT	TAAAATGGCA	AGATTATAGA	GAAAACGCCC	TTAAAAGACT	GAACGCTTTT	840

7359 AAAATCGGCT CGCATAAAAT GGAAGAATTT AGGGATAAAC AAGGGCGTTT GTGGGTAGAT 900
7360
7361 GACAGCAAAG CCACGAATAT TGATGCCACC TTACAAGCCC TAAAAAACCTT TAAAAACCAA 960

7362
7363 AAAATCCATT TGATTTTAGG GGGCGATATT AAAGGGGTCA ATTTAACCCC CCTTTTTGAA 1020

7364
7365 GAGTTTAAAA ACTATAAAAT AAGCCTTTAT GCCATAGGAT CAAGCGCTTC TATCATACAA 1080

7366
7367 GCCTTAGCGT TAGAATTTAA TGTTTCTTGT CAGGTTTGTT TGAAGTTAGA AAAAGCGGTT 1140

7368
7369 CAAGAAATTA AAAGCGTTTT ATTACAAAAT GAAGTCGCTT TGCTTTCACC TAGCGCGGCC 1200

7370
7371 AGTTTGGATC AATTTTCTTC GTATAAAGAA AGGGGTGAAA AATTCAAAGC GTTTGTTTTA 1260

7372 7373 AAAGAT 1266

7374 7375

8045

8046 8047 8048

8049

8050

8051

8052

8060

7358

(2) INFORMATION FOR SEQ ID NO:149:

111	SPOURNOR	CHARACTERISTICS:
1 1	SECUENCE	CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

8053 (ii) MOLECULE TYPE: DNA (genomic)

8054 8055 (iii) HYPOTHETICAL: NO

8056 8057 (iv) ANTI-SENSE: NO

8058 8059 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PHOSPHOMANNO PUTASE:

8065 8066 ATGATCACTG GCTCTCACAA CCCCAAAGAA TACAACGGCT TTAAAATCAC GCTCAATCAA 60 8067 8068 AACCCGTTTT ATGGCAAGGA CATTCAGGCT TTAAAAAACA CGCTTTTAAA CGCAAAGCAT 120 8069 8070 GAAATAAAGC CCCTAAAAGA AACGCCAGAG AAAGTCAATG CCCTAGAAGC GTATCATCGC 180 8071 8072 TATTTGATCA AGGATTTTAA GCATTTAAAA AATCTTAAAT ACAAAATCGC CCTGGATTTT 240 8073 8074 GGTAATGGCG TGGGGGCGTT AGGATTAGAG CCGATTTTAA AGGCTTTAAA CATTGATTTT 300

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DATE: 02/23/96 TIME: 11:35:08

	8075		
	8076	AGCAGCCTTT ATAGCGATCC TGATGGGGAT TTTCCTAACC ACCACCCAGA CCCTAGCGAA 360	
	8077		
	8078	GCGAAAAACT TAAAAGACTT AGAAAAACAC ATGCGAGAAA ACGCTATTTT AATAGGCTTT 420	
	8079		
	8080	GCTTTTGATG GCGATGCGGA TAGGATTGCG ATGCTAAGCT CTCATCATAT CTATGCGGGC 480	
	8081		
	8082	GATGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC AAGGCATCAC CCCTTTTGTG 540	
	8083		
	8084	ATCGGCGAAG TCAAATGCTC TCAAGTGATG TATAACGCAA TCAATACTTT TGGTAAGACG 600	
	8085	OMOLEGO DE 111000000 DE 0011000 LE 111001100 DE 111001100 DE 111001100 DE 111001100 DE 111001100 DE 111001100	
	8086	CTCATGTATA AAACCGGGCA TAGCAATTTA AAAATCAAGC TCAAAGAAAC TAATGCGCAT 660	
	8087	MMMCCCCCMC 122MC2CCCC CC27M2MCMMM MMM2222C22CC CCM2MMMMMCC CM2MC27C2CC CC27MC27C2CC	
	8088 8089	TTTGCGGCTG AAATGAGCGG GCATATCTTT TTTAAAGAAC GCTATTTTGG CTATGATGAC 720	
	8090	GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG AACAAAGTCC AAGCGACTTG 780	
	8091	GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG AACAAAGTCC AAGCGACTTG 780	
	8092	GAAAACACCA TTAAAAAACCT CCCCTATTCC TACACCACGC CTGAAGAAAA AATCGCCGTG 840	
	8093	OHAMACACCA TIMAMAACCI CCCCIMICC INCACCACGC CIGARGAAAA AAICGCCGIG 040	
	8094	AGCGAAGAAG AAAAATTTGA AATCATTCGC AACTTACAAG AAGCGCTTAA AAACCCGCCA 900	
	8095		
	8096	AGCCATTTCC CTACAATCAA AGAAATCATC AGCATTGATG GCGTGAGAGT GGTTTTTGAA 960	
	8097		
	8098	CATGGCTTTG GGCTTATTCG CGCAAGCAAC ACCCACCCCC TATTTAGTCA GCCGCTT 1017	
	8099		
	8100		
	8615 8616	(2) INFORMATION FOR SEQ ID NO:162:	
	8617	(i) SEQUENCE CHARACTERISTICS:	
->	8618 /	(A) LENGTH: 753 base pairs	
	8619(E: \)/	
->	8620	(A) ORGANISM: Helicobacter pylori	
	8621		
	8622	(ix) FEATURE:	
	8623	(A) NAME/KEY: misc_feature	
	8624	(B) LOCATION: 1300	
	8625	(D) OTHER INFORMATION: /note= " UDF-N-ACETYLMURAMYL-TRIPEPTIDE	
	8626	SYNTHETASE"	
	8627	(with appropriate programmer)	
	8628 8629	(xi) SEQUENCE DESCRIPTION:SEQ ID NO (214:)	
	8630	ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA 60	
	8631	ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA 60	
	8632	AGCGAAAACG AAGAAGACAT CATTAAGGAT ATTTTAAAAG GCATCAATAA TTCTTCTAAA 120	
	8633	120	
	8634	GTCATTGTAG AAAAAGACCG AAAAAAGGCC ATTTTAAACG CTTTAGAAAA TTTAAAAGAC 180	
	8635	100 TOURS INDICATED TOUR PROPERTY OF THE PROPE	
	8636	GATGAGGTGT TGTTGATTTT AGGCAAGGGC GATGAAAACA TTCAAATCTT TAAAGACAAA 240	
	8637	21V	
	8638	ACGATTTTTT TTAGCGACCA GGAAGTCGTT AAAGATTATT ATCTCAATTT AAAACAAGGA 300	
	8639		
	8640		

RAW SEQUENCE LISTING PATENT APPLICATION US/08/487,032

DATE: 02/23/96 TIME: 11:35:13

>	8641	(2) INFORMATION FOR SEQ ID NO:215:
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	8643	(i) SEQUENCE CHARACTERISTICS:
	8644	(A) LENGTH: 240 base pairs
	8645	(B) TYPE: nucleic acid
	8646	(C) STRANDEDNESS: double
	8647	(D) TOPOLOGY: circular
	8648	
	8649	(ii) MOLECULE TYPE: DNA (genomic)
	8650	and the state of t
	8651	(iii) HYPOTHETICAL: NO
	8652	
	8653	(iv) ANTI-SENSE: NO
	8654	(,
	8655	(vi) ORIGINAL SOURCE:
	8656	(A) ORGANISM: Helicobacter pylori
	8657	(A) OKSANISM. NEITCODACCET PYTOTI
	8658	(ix) FEATURE:
	8659	
		(A) NAME/KEY: misc_feature
	8660	(B) LOCATION: 1240
	8661	(D) OTHER INFORMATION: /note= "FLAGELLAR MOTOR SWITCH PROTEIN F"
	8662	
	8663	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
	8664	
	8665	GTGATGGACA AACTCACTAA AAGCTTGCAA ACGCAAAAAA ACTTCGCTTA TTTAGGCAAA 60
	8666	
	8667	ATCAAGCCCC AACAACTCGC TGATTTCATC ATTAACGAAC ACCCTCAAAC CATCGCCTTG 120
	8668	
	8669	ATTTTGGCCC ACATGGAARC CCCTAATGCG GCTGAAACTT TGAGCTATTT CCCTGATGAA 180
	8670	
	8671	ATGAAAGCCG AGATTTCCAT TAGAATGGCG AATTTTAGGC GAAATATCGC CCCAAGTGGT 240
	8672	
	8673	•
	8973	(2) INFORMATION FOR SEQ ID NO:224:
	8974	(1) International Day 10 Novillation
	8975	(i) SEQUENCE CHARACTERISTICS:
	8976	(A) LENGTH: 1263 base pairs
	8977	(B) TYPE: nucleic acid
	8978	
		(C) STRANDEDNESS: double
	8979	(D) TOPOLOGY: circular
	8980	
	8981	(ii) MOLECULE TYPE: DNA (genomic)
	8982	
	8983	(iii) HYPOTHETICAL: NO
	8984	
	8985	(iv) ANTI-SENSE: NO
	8986	
	8987	(vi) ORIGINAL SOURCE:
	8988	(A) ORGANISM: Helicobacter pylori
	8989	
		(xi) SEQUENCE DESCRIPTION: (SEQ ID NO: SEQ ID NO: 224:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/487,032

DATE: 02/23/96 TIME: 11:35:17

					•		
					j	INPUT SET: S892	4.raw
8991 8992	ATGAAAGGTT	TAACAATGAA	AAAATTAGTT	TTTAGCATGC	TTTTATGTTG	TAAAAGCGTG	60
8993 8994	TTTGCAGAGG	GGGAAACTCC	TTTGATTGTC	AATGACCCAG	AAACCCATGT	AAGTCAAGCC	120
8995 8996	ACTATCATAG	GCAAAATGGT	AGATAGTATC	AAAAGATACG	AAGAGATTAT	TTCTAAGGCT	180
8997 8998	CAAGCTCAAG	TCAATCAGTT	ACAAAAAGTC	AATAACATGA	TAAATACGAC	TAATTCTTTG	240
8999 9000	ATTAGTAGTA	GTGCTATCAC	TTTAGCCAAT	CCTATGCAAG	TTTTACAAAA	CGCTCAGTAT	300
9001 9002	CAAATAGAGA	GCATTAGATA	CAACTATGAG	AATTTAAAGC	AAAGCATAGA	AAATTGGAAC	360
9003 9004	GCACAAAATT	TGTTAAGAAA	CAAATACTTA	CAGCAACAAT	GCCCTTGGCT	TAATGTCAAT	420
9005 9006	GCTCTTACTA	ACAATAAGAT	TGTCAATCTT	AAAGATCTCA	ATAACCTAAT	CACCAAAAAT	480
9007 9008	GGCGAACAAA	CCCAAACCGC	AAGAGATGTG	CAAAATCTCA	TTCAGTCCAT	TAGTGGCAGT	540
9009 9010	GGCTATGGAA	ACATGCAATC	ACTTGCTGGG	GAATTGAGTG	GTAGAGCGTG	GGGGGAAATG	600
9011 9012	TTGTGTAAAA	TGGTAAACGA	TAGTAATTAT	GAAAGCGAGC	AAGCTCTTTT	AGCAACAGGC	660
9013 9014	AATAACCCAG	AAGAGCAAAA	ACGAAGATTT	TTGCTTAGAG	TAAAGAAAA	GGTTAATGAT	720
9015 9016	AATAAGCAGT	TAAAAGATAA	ACTTGACCCA	ТТТСТААААА	GACTTGATGT	CCTACAAACT	780
9017 9018	GAGTTTGGTG	TAACTGACCC	TACAGCTAAC	CATAATAAGC	AAGGGATACA	TTATTGCACA	840
9019 9020	GAAAATAAAG	AGACAGGTAA	ATGCGACCCT	ATTAAAAATG	TATTTAGGAC	AACTCGCTTA	900
9021 9022	GATAACGAAT	TAGAACAAGA	AATCCAAACG	CTCACACTTG	ATTTAATCAA	AGCCTCCAAT	960
9023 9024	AAAGACGCTC	AAAGCCAAGC	CTACGCAAAT	TTCAATCAAA	GGATTAAATT	ACTTACTCTA	1020
9025 9026	AAATATTTAA	AAGAAATTAC	CAATCAAATG	СТСТТТТТАА	ATCAAACAAT	GGCAATGCAA	1080
9027 9028	AGCGAGATTA	TGACAGATGA	TTATTTTAGG	CAAAATAATG	ATGGCTTTGG	GGAAAAAGAA	1140
9029 9030	AACCATATAG	ACGAACAATT	AACGCAAAAA	AGAATAAACG	AAAGAGAAAG	AGCTAGAATA	1200
9031 9032	TACTTTCAAA	ACCCTAATGT	TAAATTTGAC	CAATTTGGCT	TTCCCATTTT	TAGTATATGG	1260
9033 9034	GAT						1263
9035 9036							
9101	(2) INFORM	ATION FOR SE	EQ ID NO:22	7:			
9102	/ d \	201151105 01111		~ .	ا تہ	1560	0111
9103 9104		EQUENCE CHAP (A) LENGTH:		o ;	7		ou any
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/487,032

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Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the Federal Register (55 FR 18230) on May 1, 1990, and in the PTO Official Gazette (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software will be available via computer downloading (details below). Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO Official Gazette.

The software can be accessed/requested in the following locations:

- Dial-up access to the Patent and Trademark Office Bulletin Board System. Phone number: 703-305-8950 Cost: Free-of-charge
- Dial-up access through the Internet. FTP site: ftp.uspto.gov Login as "anonymous". Software is in directory /pub/checker Cost: Free-of-charge
- 3) For diskette copies, telephone requests to 703-308-0322. Cost: \$25.00

For Further Information Contact: Meredith Beckhardt at 703-308-4212.

Team 6

CRF Diskette Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following CRF diskette:
Application Serial Number: 08/487,032 Filing Date: 6/7/95
Filing Date: Q(+(\gamma))
Classification:
Date Reviewed by STIC: 223 196
Point-of-Contact / Telephone No: Meredith Beckhardt 703-308-4212
Nature of Problem:
The CRF diskette was: Damaged Unreadable — See OHacked Only parts of Blank (no files present on the floppy disk) the file could be read.
A computer virus was detected on the diskette. The STIC will not process the diskette through the Data Capture System.
Name of the virus:
The CRF diskette contains an error that disrupts normal processing, as explained below:
☐ The Sequence Listing was not converted into ASCII (DOS) text
See attached pages for clarification>
Other: